IncA/mycHIS IncB/mycHIS IncBAhydro

Figur

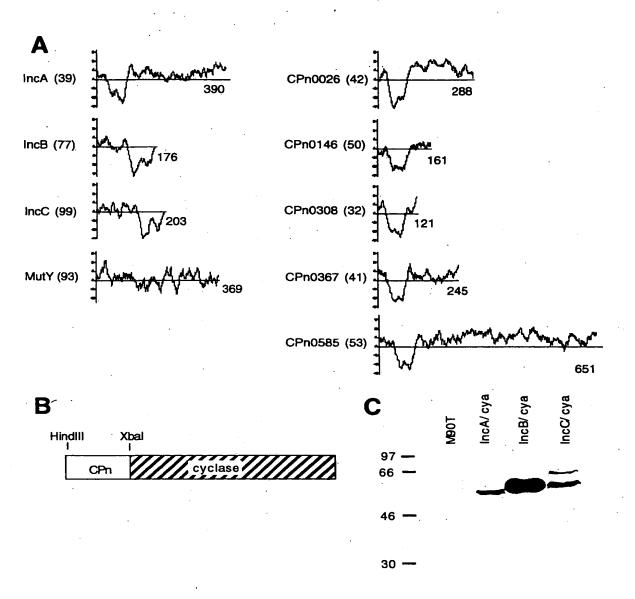


Figure 2

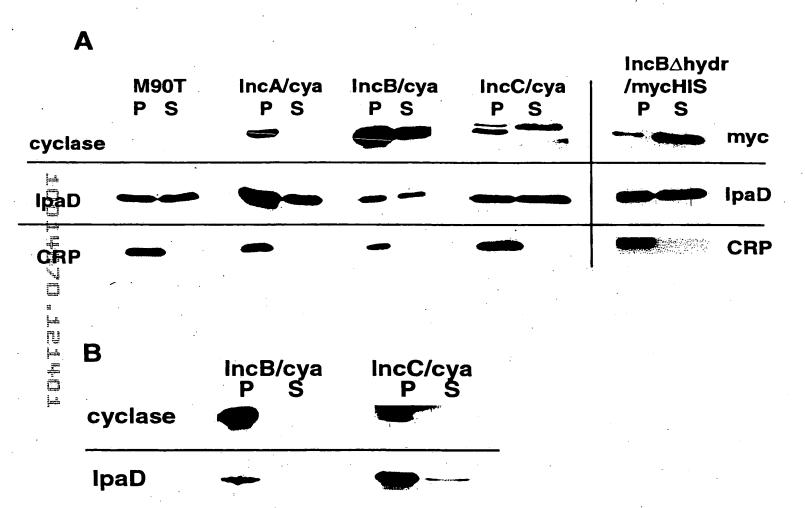


Figure 3

MutY/cya P S IncA/cya IncC/cya P S cyclase

IpaD

CRP

Figure 4

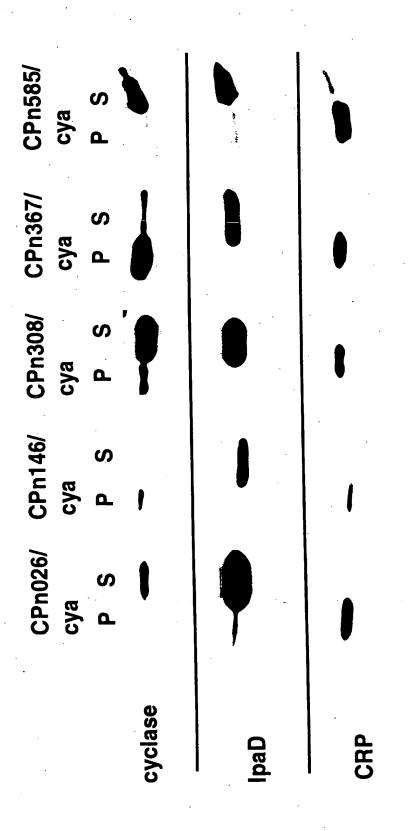


Figure 5

Figure 1: Full-length Sequence of C. pneumoniae 76kDa Gene.

3			T				•									
ataa	aato	ett !	taaa	aaca	gg ct	tege	attaa	a tta	attag	gtga	gago	ettt	tt 1	ttat	ttttt	60
ataa	taaa	aac 1	taaaa	gati	tt ti	tatta	ațtt	t ttg	gagti	ttt				cct Pro		115
							aca Thr									163
							agt Ser									211
caa Gln	aga Arg	ata Ile 40	gca Ala	ggt Gly	Ala \	gaa Glu	gct Ala 45	aag Lys	cct Pro	aaā Lys	gáa Glu	tct Ser 50	aag Lys	acc Thr	gat Asp	259
tct Ser	gta Val 55	gag Glu	cga Arg	tgg Trp	agc\ Ser	Ile (60.	ttg Leu	cgt Arg	tct Ser	gca Ala	gtg Val 65	aat Asn	gct Ala	ctc Leu	atg Met	307
							att Ile									355
							gac Asp									403
							gat Asp									451
Tyr	Asp	Thr 120	Ile	Phe	Thr	Ser	aca Thr 125	Ser	Leu	Āla	Asp	11e 130	Gln	Ala	Ala	499
ttg Leu	gtg Val 135	agc Ser	ctc Leu	cag Gln	gat Asp	gct Ala 140	gtc Val	act Th	aat Asn	ata Ile	aag Lys 145	gat Asp	aca Thr	gcg Ala	gct Ala	547
							gct Ala									595
							caa Gln									643
							gac Asp									691

Figure 1 (continued)

	_		٠.		• -												
g: A:	ac sp	ctc Leu	tta Leu 200	cag Gln	gct [.] Ala	gct Ala	ctt Leu	ctc Leu 205	caa Gln	tct Ser	gta Val	gca Ala	aac Asn 210	aat Asn	aac Asn	aaa Lys	739
g A	ca la	gct Ala 215	gag Glu	ctt Leu	ctt Leu	aaa Lys	gag Glu 220	atg Met	caa Gln	gat Asp	aac Asn	cca Pro 225	gta Val	gtc Val	cca Pro	gly aaa	787
Ŀ	aa ys 30	acg Thr	cct Pro	gca Ala	att Ile	gct Ala 235	caa Gln	tct Ser	tta Leu	gtt Val	gat Asp 240	cag Gln	aca Thr	gat Asp	gct Ala	aca Thr 245	835
g A	cg la	aca Thr	cag Gln	ata Ile	gag Glu 250	aaa Lys	gat Asp	gga Gly	aat Asn	gcg Ala 255	att Ile	agg Arg	gat Asp	gca Ala	tat Tyr 260	ttt Phe	883
9 A	ca la	gga Gly	cag Gln	aac Asn 265	gct Ala	agt Ser	gga Gly	gct Ala	gta Val 270	gaa Glu	aat Asn	gct Ala	aaa Lys	tct Ser 275	aat Asn	aac Asn	931
a S	gt er	ata Ile	agc Ser 280	aac Asn	ata Ile	gat Asp	tca Ser	gct Ala 285	aaa Lys	gca Ala	gca Ala	atc Ile	gct Ala 290	act Thr	gct Ala	aag Lys	979
a T	ca hr	caa Gln 295	ata Ile	gct Ala	gaa Glu	gct Ala	cag Gln 300	aaa Lys	aag Lys	ttc Phe	ccc Pro	gac Asp 305	tct Ser	cca Pro	att Ile	ctt Leu	1027
G	aa ln 10	gaa Glu	gcg Ala	gaa Glu	caa Gln	atg Met 315	gta Val	ata Ile	cag Gln	gct Ala	gag Glu 320	aaa Lys	gat Asp	ctt Leu	aaa Lys	aat Asn 325	1075
a I	tc le	aaa Lys	cct Pro	gca Ala	gat Asp 330	ggt Gly	tct Ser	gat Asp	gtt Val	cca Pro 335	aat Asn	cca Pro	gga Gly	act Thr	aca Thr 340	gtt Val	1123
g	ga ly	ggc Gly	tcc Ser	aag Lys 345	caa Gln	caa Gln	gga Gly	agt Ser	agt Ser 350	att Ile	ggt Gly	agt Ser	att Ile	cgt Arg 355	gtt Val	tcc Ser	1171
a M	tg let	ctg Leu	tta Leu 360	gat Asp	gat Asp	gct Ala	gaa Glu	aat Asn 365	gag Glu	acc Thr	gct Ala	tcc Ser	att Ile 370	ttg Leu	atg Met	tct Ser	1219
g	lgg 1	ttt Phe 375	cgt Arg	cag Gln	atg Met	att Ile	cac His 380	atg Met	ttc Phe	aat Asn	acg Thr	gaa Glu 385	aat Asn	cct Pro	gat Asp	tct Ser	1267
G	aa ln 90	gct Ala	gcc Ala	caa Gln	cag Gln	gag Glu 395	ctc Leu	gca Ala	gca Ala	caa Gln	gct Ala 400	aga Arg	gca Ala	gcg Ala	aaa Lys	gcc Ala 405	1315
9 A	ıct	gga Gly	gat Asp	gac Asp	agt Ser 410	gct Ala	gct Ala	gca Ala	gcg Ala	ctg Leu 415	gca Ala	gat Asp	gct Ala	cag Gln	aaa Lys 420	gct Ala	1363

Figure 1 (continu d)

Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr 570 575 580 tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt 1891 Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu 585 590 595 tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt 1939 Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 600 605 605 gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa 1987 Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 625	Ŭ		•														
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro 445 CCC gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys 465 acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly 470 485 tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cqa aat Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn Soo gat gcg act cgt gat gtg ata aac aat gat agt acc ccc gct ctc aca Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr Soo gat ccc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Soo gat caa gcc ctc gct agg gtg st tct Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly Soo gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag acc at acc Asp Wal Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Soo cag tcg act cct caa gcg aat aat gag gag atc aga caa aag ctt acc Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr Soo cag tcg gat gtc caa ag cct cca cag ttt ggc tat cct tat gtg caa ctt Cgn Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu Sor Ash Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 615 ccc gaa gga ctc agg aca gca gcd gcd gcd aat aaa gca ctt tcc ttt gaa Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu Ccc gca gaa ctc ct tat ttt tat cag cag gtc gtc cat acc ctc tcc Cac gca ctc tcc tat ttt tat cag cag gtc gtc ctc tat tcc Cac gca ctc ctc tat ttt tat cag cag gtc ctc gtc aat acc Cac ctc tat gaa cat ctc tag ccc Cac gca ctc ctc tat gcc cac ctc Cac gca gca gca ctc acc ctc cac ctc ccc Cac gca gca gca ccc ccc ccc Cac ctc ccc ccc Cac ccc ccc ccc Cac ccc cccc Cac ccc Cac cc	tta Leu	gaa Glu	gcg Ala	Ala	cta Leu	ggt Gly	aaa Lys	gct Ala	Gly	caa Gln	caa Gln	cag Gln	Gly	TIE	ctc Leu	aat Asn	1411
## Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys 465 ## A65 ## A65 ## A66 ## A66 ## A67 ## A68 ## A67 ## A67 ## A67 ## A68 ## A67 ## A68 ## A67 ## A68 ## A67 ## A68 ## A68 ## A67 ## A68 ## A66 ## A66 ## A79 ## A1 ## A79 ## A	gct Ala	tta Leu	Gly	cag Gln	atc Ile	gct Ala	tct Ser	Ala	gct Ala	gtt Val	gtg Val	agc Ser	Ala	gga Gly	gtt Val	cct Pro	1459
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln 11e Ser Ala 2475 tat gat gct tac aaa tcc atc aat gat gct tat ggt agg gca cga aat 1603 Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn 500 gat gcg act cgt cct aga gca cga aca gaa gct cga aca gaa gct Cga aca gca aca gca gaa gcd Cga aca aca gca gca gca gcg aca gca gca g	ccc Pro	Ala	gca Ala	gca Ala	agt Ser	tct Ser	Ile	61A 888	tca Ser	tct Ser	gta Val	Lys	cag Gln	ctt Leu	tac Tyr	aag Lys	1507
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ash Arg Ash Ash <td>Thr</td> <td>tca Ser</td> <td>aaa Lys</td> <td>tct Ser</td> <td>aca Thr</td> <td>Gly</td> <td>tct Ser</td> <td>gat Asp</td> <td>tat Tyr</td> <td>aaa Lys</td> <td>Thr</td> <td>cag Gln</td> <td>ata Ile</td> <td>tca Ser</td> <td>gca Ala</td> <td>GIA</td> <td>1555</td>	Thr	tca Ser	aaa Lys	tct Ser	aca Thr	Gly	tct Ser	gat Asp	tat Tyr	aaa Lys	Thr	cag Gln	ata Ile	tca Ser	gca Ala	GIA	1555
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr 505 cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aca l699 Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly 530 gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga 1747 Asp Cln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly 535 gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc gln Ser Asn Asp Cln Ala Asn Asn Asn Clu Glu Glu Glu Ile Arg Cln Ile Asp Asn Asp Ser Ala Val Thr Lys Pro Pro Cln Phe Gly Tyr Pro Tyr Val Gln Leu Ser Leu Phe Ile Gln Cln Cln Cln Cln Cln Cln Cln Cln Cln C	tat Tyr	gat Asp	gct Ala	tac Tyr	Lys	tcc Ser	atc	aat Asn	gat Asp	Ala	tat Tyr	ggt Gly	agg Arg	gca Ala	Arg	aat Asn .	
Ser Val Ser Val Ser Ser Val Ser Ser Ser Ala Ser Ser Ala Val Thr Ser Ala Val Thr Ser Ser Ala Val Thr Ser Thr Ser Ala Val Thr Ser Thr Ser Thr Ser Thr Ser Ala Val Thr Ser Thr Ser Thr Ser Ala Val Thr Ser Thr Ser Thr Ser Thr Ala Ala Ser Ala Ser Ala Ser Thr Ser Ala Ala Ser Ala Ser Ala Ser Arg Thr Ala Ala Ser Thr Ala Ala Ser Thr Ser Th	gat Asp	gcg Ala	act Thr	Arg	gat Asp	gtg Val	ata Ile	aac Asn	Asn	gta Val	agt Ser	acc Thr	ccc Pro	ATA	ctc Leu	aca Thr	1651
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly 535 gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc Ile 560 cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca file 560 cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca file 570 tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt Thr S80 tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt Thr S80 tct aat gac tct aca cag aag ttc ata gct Thr S95 tct aat gac tct aca cag aag ttc ata gct aca agt tta gct S95 tct aat gac tct aca cag aag ttc ata gct aca att gaa agt ttg ttt S95 tct aat gac tct aca cag aag ttc ata gct aca tta gaa agt ttg ttt S95 ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe G15 gct gaa gga tct agg aca gca gct gaa ata aca gca ctt tcc ttt gaa Ala Glu Gly G15 acg aca tcc ttg ttt att cag cag gtg ctg gtc acat atc ggc tct cta cta gac acat acc gac gtg cag acc gtc gac acc acc acc gac gtg ctg gtc acc acc ctt ctc ttc gac leu Ser Phe Glu 625 acg acc tcc ttg ttt att cag cag gtg ctg gtc acat atc ggc tct ctc cta cac acc acc cag acc ctc tcc ttc gac leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 645	cga Arg	tcc Ser	Val	cct Pro	aga Arg	gca Ala	cga Arg	Thr	gaa Glu	gct Ala	cga Arg	gga Gly	Pro	gaa Glu	aaa Lys	aca Thr	1699
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Tie Tie 550 cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Tle Arg Gln Lys Leu 570 tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu 585 tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt Ser Asn Asp Ser Thr Gln Lys Phe Tle Ala Lys Leu Glu Ser Leu Phe 600 gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa Ala Glu Gly Ser Arg Thr Ala Ala Glu Tle Lys Ala Leu Ser Phe Glu 615 acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta Thr Asn Ser Leu Phe Tle Gln Gln Val Leu Val Asn Tle Gly Ser Leu 645	gat Asp	Gln	gcc Ala	ctc Leu	gct Ala	agg Arg	Val	att Ile	tct Ser	ggc	aat Asn	Ser	aga Arg	act Thr	ctt Leu	gga Gly	1747
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr 570 580 tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt 1891 Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu 585 tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt 1939 Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 600 gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa 1987 Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 625 acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta 2035 Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 645	Asp	Val	tat Tyr	agt Ser	caa Gln	Val	tcg Ser	gca Ala	cta Leu	caa Gln	Ser	Val	atg Met	cag Gln	atc Ile	116	1795
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu 585 tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 600 gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 625 acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 645	cag Gln	tcg Ser	aat Asn	cct Pro	Gln	Ala	aat Asn	aat Asn	gag Glu	Glu	Ile	aga Arg	caa Gln	aag Lys	ren	Inr	1843
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 600 605 610 gct gaa gga tct agg aca gct gaa ata aaa gca ctt tcc ttt gaa Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 625 acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 645	tcg Ser	gca Ala	gtg Val	Thr	Lys	cct Pro	cca Pro	cag Gln	Phe	Gly	tat Tyr	cct Pro	tat Tyr	. vai	GIT	ctt Leu	1891
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 615 620 625 acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 645	tct Ser	aat Asn	Asp	Ser	aca Thr	cag Glr	aaç Lys	Phe	: Ile	gct Ala	aaa Lys	tta Lei	ı Gli	ı ser	tto Lev	ttt Phe	1939
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu	gct Ala	Glu	GT2	tct Ser	agg Arg	g aca	Ala	a Ala	gas a Glu	a atá	a aaa e Lys	s Ala	a Lev	t tco 1 Sei	ttt Phe	gaa Glu	1987
	Thi	. Asr	tco Sei	tti Lev	g ttt 1 Phe	e Ile	e Glr	g cag n Glr	g gtg n Val	g ctg L Lev	ı Val	l As	t ato	e Gly	tot / Se	r Leu	2035

Figure 1 (continued)

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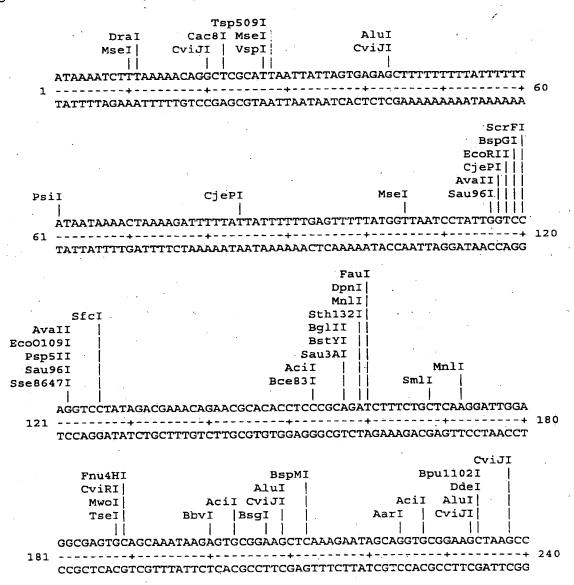
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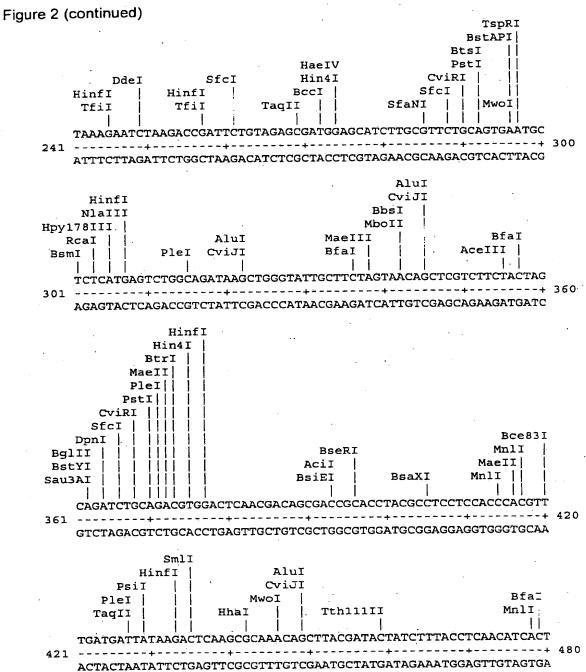
aataaataaa aga

2156

2083

Figure 2: Restriction enzyme map of C. pneumoniae 76kDa gene.





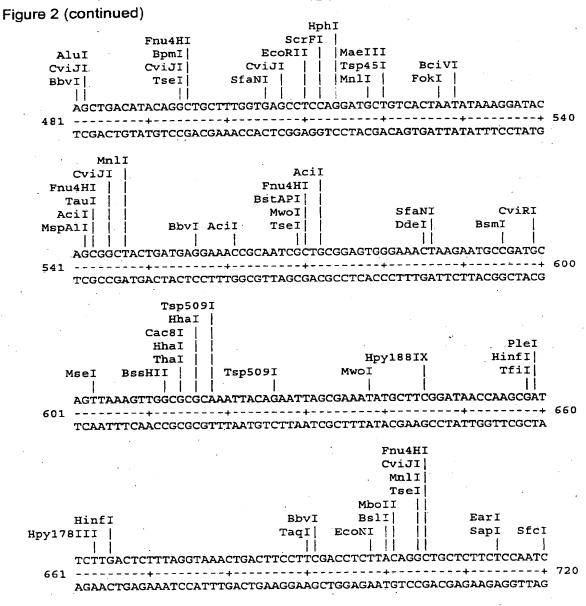


Figure 2 (continued)

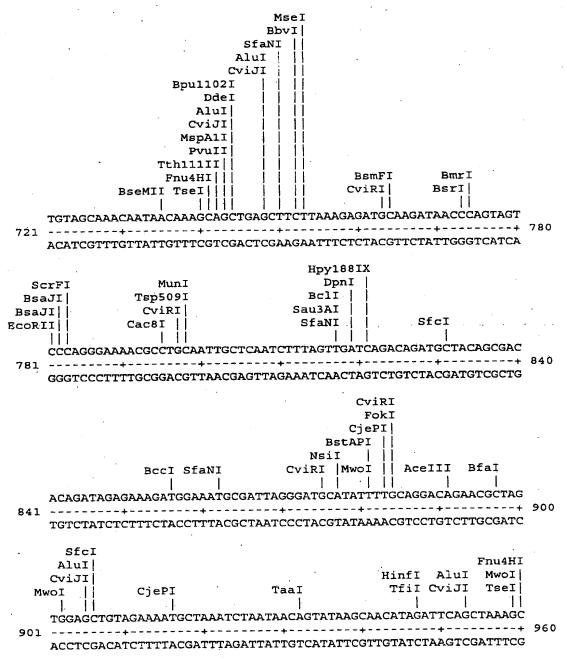


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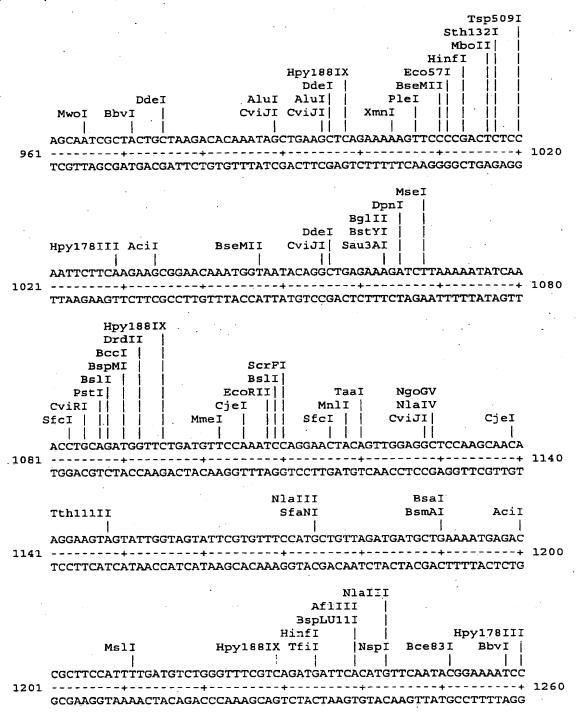


Figure 2 (continued)

arc 2 (borningsa)			•	
Bs _l Fnu4HI SmlI AluI HinfI CviJI	GGAGCTCGCAG	CACAAGCTAGAGCA	BbvI BbvI MspAlI Acil Fnu4HI TauI CviJI MwoI HwoI GCGAAAGCCGCTGG	20
Car Hae Mw Hha Eco47III PstI SfaNI BpmI Fnu4HI CviRI MwoI TseI Fnu4HI Fnu4HI Fnu4HI Fnu4HI Fnu4HI TseI TseI TseI TseI TseI TseI TseI TseI TseI Fnu4HI TseI Fnu4HI TseI TseI Fnu4HI TseI Fnu4HI TseI TseI	C8I II OI I I I I I I I I I I I I I I	AluI CviJI HindIII F MWOI BSIX EI BseMI MWO	BfaI CviJI nu4HI TauI AciI I I GAAGCGGCTCTAGG	
TCTACTGTCACGACGACGTCG AluI CviJI TAAAGCTGGGCAACAACAGGG	CGACCGTCTAC	CGAGTCTTTCGAAAT DpnI Sau3AI BbvI	Fnu4HI MwoI TseI 	\$ 8 C
1201			14	440

Figure 2 (continued)

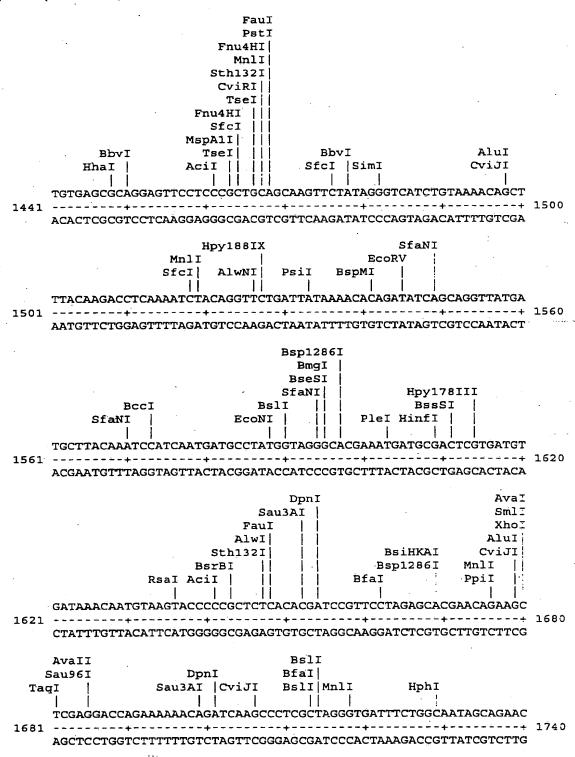


Figure 2 (continued)

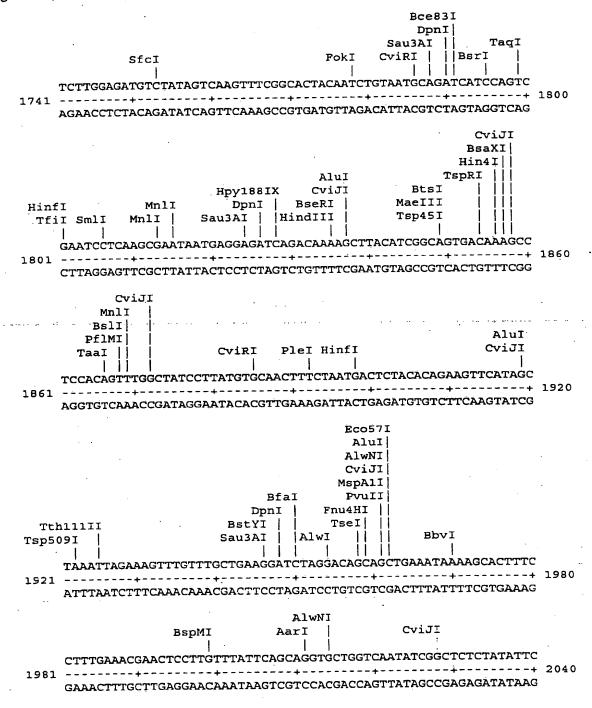


Figure 2 (continued)

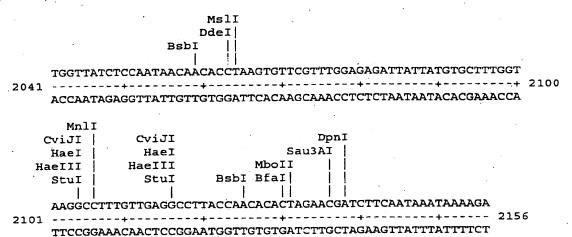


Figure 3: Sequence Containing Truncated Version of C. pneumoniae 76kDa Gene; (nucleotides 1 to 665 and 2122 to 2238 are unrelated to the 76kDa Gene).

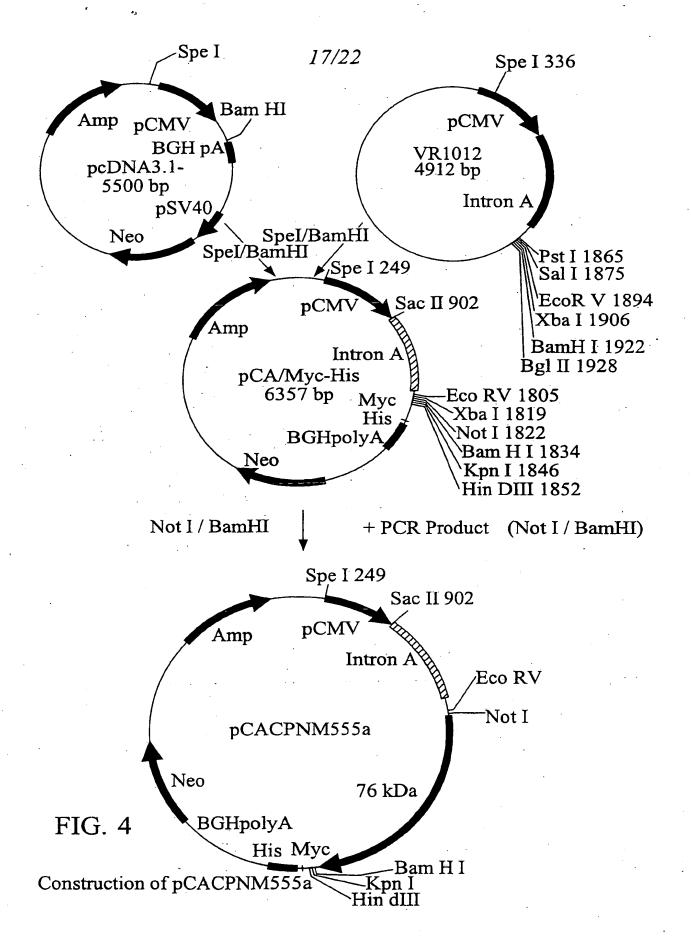
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tttt	ttgt	ga a	atgt	agtg	t tg	tcga	ctgg	aac	acat	tcg	ttcc	ttca	ga a	acct	ccact	120
acag	raaaa	ag c	etget	acaa	a cg	ctat	gaaa	tac	aaat	act	gtgt	ttgg	ca g	gtggc	tcgtc	180
ggaa	agca	ta g	gtcag	gttc	c tt	ggat	caat	gga	caga	aaa	agco	tcta	ta t	cttt	atgga	240
gctt	tctt	aa t	gaac	cctt	t ag	caaa	ggct	acg	aaga	cța	cgtt	aaat	gg a	aaaag	aaaac	300
ctaç	ıcttg	gt t	tatt	ggag	g aa	cttt	aggg	gga	ctca	gaa	aago	tgga	ga c	tggt	ctgcc	360
acag	tacg	tt a	atgag	jtatg	t cg	aago	cttg	teg	gtto	cag	aaat	agat	gt t	tcag	ggatt	420
ggco	gtgg	ta a	attta	ttaa	a gt	tttg	gttc	gcc	caag	caa	ttgc	tgct	aa c	ctatg	atcct	480
aaag	aggc	ta a	atggt	ttta	c aa	atta	taaa	gga	tttt	ccg	ctct	atat	at g	gtatg	gcatc	540
acag	attc	tc t	atca	ttca	g ag	rctta	tggg	gct	tact	cca	aacc	agca	aa c	gata	aactc	600
ggca	ıgtga	tt t	tact	ttcc	g aa	agtt	tgat	cta	ggta	taa	tttc	agcg	rt t	taag	tcaaa	660
tttt	aata	aa a	atctt	taaa	a ac	aggo	tege	att	aatt	att	agto	agag	ict t	tttt	tttat	720
tttt	tata	at a	aaaa	taaa	a ga	tttt	tatt	att	ttt	gag	tttt	t at	g gt	tt aa	t cct	777
												Me	+ 37=	∍l λe	n Pro	
					-							Me	t Va 1	al As	n Pro	
att Ile 5	ggt Gly	cca Pro	ggt Gly	cct Pro	ata Ile 10	gac Asp	gaa Glu	aca Thr	gaa Glu	cgc Arg 15	aca Thr	cct	1 ccc	el As gca Ala	gat	825
Ile 5 ctt	Gly	Pro gct	Gly	Progga	Ile 10 ttg	Asp	Glu	Thr	Glu	Arg 15 gca	Thr	cct Pro	1 ccc Pro	gca	gat Asp 20 gaa	825 873
Ile 5 ctt Leu	tct Ser	Pro gct Ala	Gly caa Gln ata	gga Gly 25	Ile 10 ttg Leu	Asp gag Glu gcg	gcg Ala gaa	Thr agt Ser gct	gca Ala 30	Arg 15 gca Ala cct	Thr aat Asn	cct Pro aag Lys	ccc Pro agt Ser	gca Ala gcg Ala	gat Asp 20 gaa Glu acc	
Ile 5 ctt Leu gct Ala	tct Ser caa Gln	gct Ala aga Arg	caa Gln ata Ile 40	gga Gly 25 gca Ala	Ile 10 ttg Leu ggt Gly	gag Glu gcg Ala	Glu gcg Ala gaa Glu atc	Thr agt Ser gct Ala 45	gca Ala 30 aag Lys	Arg 15 gca Ala cct Pro	Thr aat Asn aaa Lys	cct Pro aag Lys gaa Glu	ccc Pro agt Ser tct Ser 50	gca Ala gcg Ala 35	gat Asp 20 gaa Glu acc Thr	873
ctt Leu gct Ala gat Asp	tct Ser caa Gln tct Ser	gct Ala aga Arg gta Val 55	Cly caa Gln ata Ile 40 gag Glu	gga Gly 25 gca Ala cga Arg	Ile 10 ttg Leu ggt Gly tgg Trp	gag Glu gcg Ala agc Ser	gcg Ala gaa Glu atc Ile 60	Thr agt Ser gct Ala 45 ttg Leu att	gca Ala 30 aag Lys cgt Arg	Arg 15 gca Ala cct Pro tct Ser	Thr aat Asn aaa Lys gca Ala agt	cct Pro aag Lys gaa Glu gtg Val 65 aac	ccc Pro agt Ser tct Ser 50 aat Asn	gca Ala gcg Ala 35 aag Lys	gat Asp 20 gaa Glu acc Thr ctc Leu	873 921

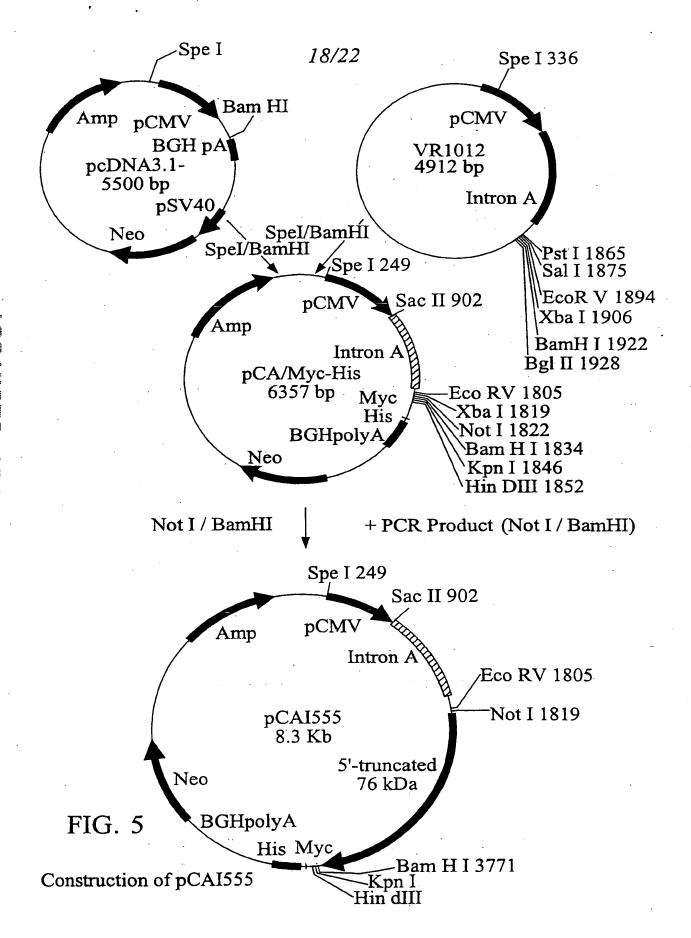
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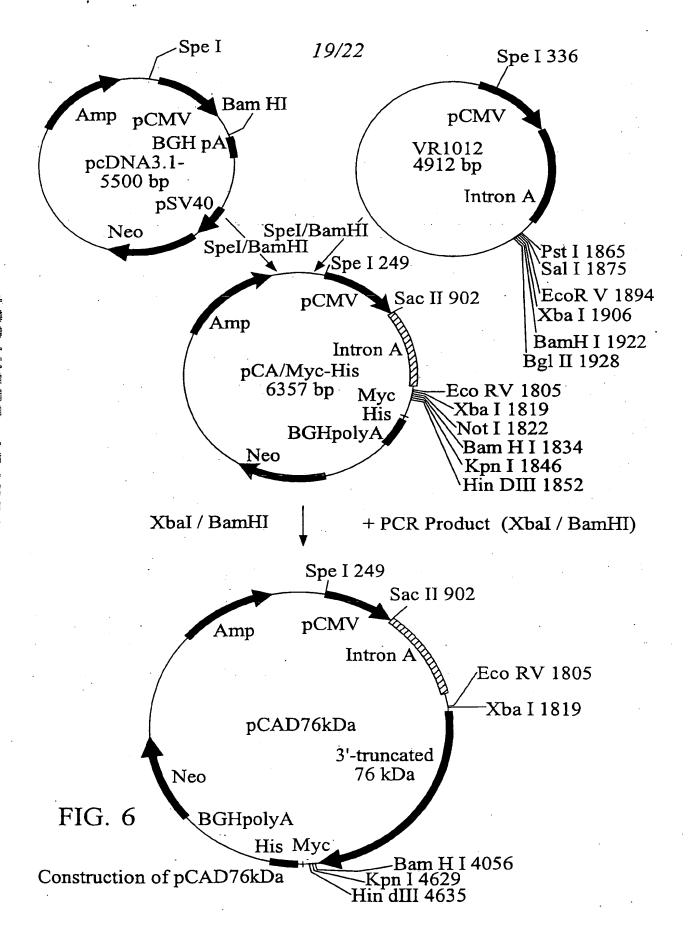
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Figure 3 (continued)

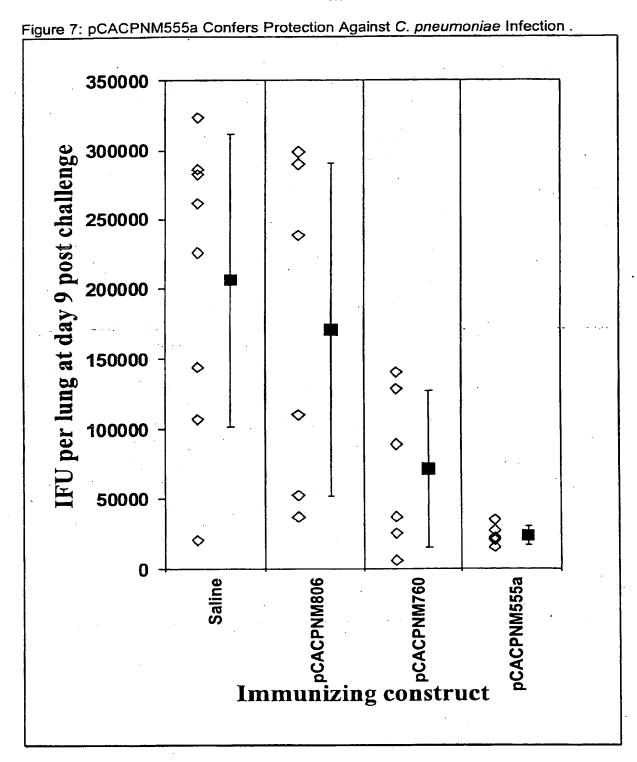
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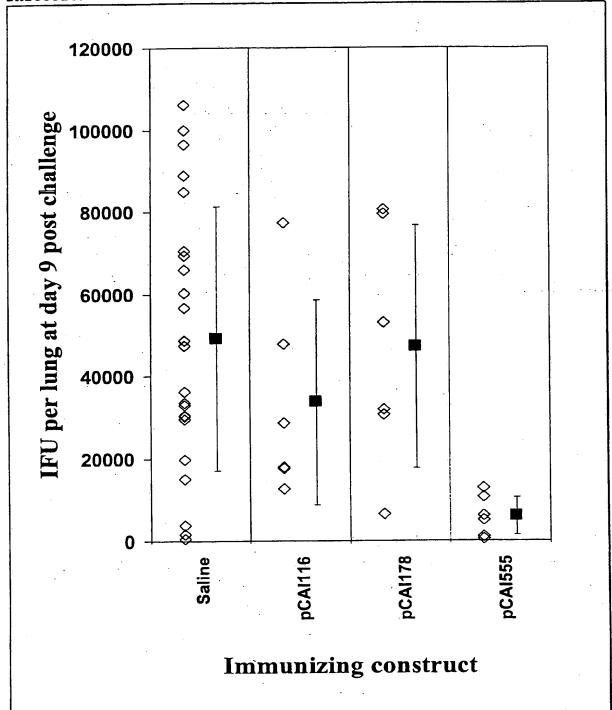


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Figure 8: pCAI555 Confers Protection Against C. pneumoniae Infection.



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Figure 9: pCAD76kDa Confers Protection against C. pneumoniae Infection.

